

Supplementary materials

Supplementary Table S1. Primers used in this study

Primer	Sequence (5'-3')	Application
TRAF1-ORF-F	ATGGCTTTAGCAGCGCCTGT	ORF cloning
TRAF1-ORF-R	TCAAGATGAAGAGTCCACCACACA	ORF cloning
TRAF2a-ORF-F	ATGTTTCATTATAGCTCATGCTTT	ORF cloning
TRAF2a-ORF-R	TAAAAGGCCAGTGAGGTCAACAATG	ORF cloning
TRAF2b-ORF-F	ATGTTTCATTATAGCTCATGCTTTCT	ORF cloning
TRAF2b-ORF-R	TTAAAGGCCAGTGAGGTCAACA	ORF cloning
TRAF3-ORF-F	ATGTCCTTGCCGCACCGT	ORF cloning
TRAF3-ORF-R	TCATGGGTGTCAGGCAGGTCTG	ORF cloning
TRAF4a-ORF-F	ATGCCCCGGCTACGACTATAAG	ORF cloning
TRAF4a-ORF-R	TCAAGCCATGATCTTTTGTGG	ORF cloning
TRAF4b-ORF-F	ATGCCTGGTTTAGATTACAAGTTTCT	ORF cloning
TRAF4b-ORF-R	TTAGTTGATTATTCTCTGCACCACAT	ORF cloning
TRAF5-ORF-F	ATGGCAGCTGAGGAGAATGAAT	ORF cloning
TRAF5-ORF-R	CTACAAATCCTCCAACCCTGTT	ORF cloning
TRAF6-ORF-F	ATGGCATCATGTAGTGACATGC	ORF cloning
TRAF6-ORF-R	TCAGAGAGATGGTTCAGGTCCTC	ORF cloning
TRAF7-ORF-F	ATGAGCTCCGGTAAATCGCACT	ORF cloning
TRAF7-ORF-R	TTAGCAGGTCCACACCTTCACG	ORF cloning
TRAF1-RT-F	ATAAACGGAGACGGAGTGGA	qRT-PCR
TRAF1-RT-R	GGAACGATACGGACGAGAGGT	qRT-PCR
TRAF2a-RT-F	ATGGAGGCTTACAACCGC	qRT-PCR
TRAF2a-RT-R	CCTCTTCTTGGAAGTCCG	qRT-PCR
TRAF2b-RT-F	GTGGACATCGTTTCTGCGT	qRT-PCR
TRAF2b-RT-R	TGCTGACCCTCGTAATCTTTC	qRT-PCR
TRAF3-RT-F	AATCATTGTTTCGTTTCCATCCAT	qRT-PCR
TRAF3-RT-R	ACTCGTGCTCCCTAATTTCTG	qRT-PCR
TRAF4a-RT-F	TGCTGCCTGGCGAATACG	qRT-PCR
TRAF4a-RT-R	GGCTGCCACTGGGTTTCTG	qRT-PCR
TRAF4b-RT-F	TATGCTGGGATTCGGCTACC	qRT-PCR
TRAF4b-RT-R	GCTTTGATGAAGATGGCGTTG	qRT-PCR
TRAF5-RT-F	AAACGAAGCAAAGTGAAAGTC	qRT-PCR
TRAF5-RT-R	CTCAGCATCCAGAACATTACG	qRT-PCR
TRAF6-RT-F	TTCGGGGTCAGTTGTCGT	qRT-PCR
TRAF6-RT-R	ATGTTTCGGATGGGGTG	qRT-PCR
TRAF7-RT-F	TGGTGGTGAATAACATCGCTG	qRT-PCR
TRAF7-RT-R	GTTTGACGGTGAAAGGGCA	qRT-PCR
Ex-TRAF1-F	CCGGAATTCATGGCTTTAGCAGCGCCTGT	Plasmid construction
Ex-TRAF1-R	CGGGGTACCAGATGAAGAGTCCACCACACACT	Plasmid construction
Ex-TRAF2a-F	CCGGAATTCATGTTTCATTATAGCTCATGCTTT	Plasmid construction

Primer	Sequence (5'-3')	Application
Ex-TRAF2a-R	CGGGGTACCAAGGCCAGTGAGGTCAACAATG	Plasmid construction
Ex-TRAF2b-F	CCGCTCGAGATGGCACGTCCATCTTTGC	Plasmid construction
Ex-TRAF2b-R	CGGGGTACCAAGTCCTGTGAGATCTACGATCGC	Plasmid construction
Ex-TRAF3-F	CCGCTCGAGATGTCCTTGCCGCACCGT	Plasmid construction
Ex-TRAF3-R	CGGGGTACCTGGGTCAGGCAGGTCTGAA	Plasmid construction
Ex-TRAF4a-F	CCGGAATTCATGCCCCGGCTACGACTATAAGT	Plasmid construction
Ex-TRAF4a-R	CGGGGTACCAGCCATGATCTTTTGTGGGATC	Plasmid construction
Ex-TRAF4b-F	CCGGAATTCATGCCTGGTTTAGATTACAAGTTT	Plasmid construction
Ex-TRAF4b-R	CGGGGTACCGTTGATTATTCTCTGCACCACATC	Plasmid construction
Ex-TRAF5-F	CCGCTCGAGATGGCAGCTGAGGAGAATGAA	Plasmid construction
Ex-TRAF5-R	CGGGGTACCCAAATCCTCCAACCCTGTTGT	Plasmid construction
Ex-TRAF6-F	CCGGAATTCATGGCATCATGTAGTGACATGCAC	Plasmid construction
Ex-TRAF6-R	CGGGGTACCGAGAGATGGTTCAGGTTCTCGAGG	Plasmid construction
Ex-TRAF7-F	CCCAAGCTTATGAGCTCCGGTAAATCGCACT	Plasmid construction
Ex-TRAF7-R	CGGGGTACCGCAGGTCCACACCTTCACG	Plasmid construction
β-actin-F	TCCCTGTATGCCTCTGGTGGT	Internal reference
β-actin-R	AAGCTGTAGCCTCTCTCGGTC	Internal reference

Supplementary Table S2. List of vertebrate species and the accession numbers of their TRAF amino acid sequences used in this study

No.	Species name	Gene name	Accession no.
1	<i>Homo sapiens</i>	TRAF1	NP_005649.1
		TRAF2	NP_066961.2
		TRAF3	NP_003291.2
		TRAF4	NP_004286.2
		TRAF5	NP_001306136.1
		TRAF6	NP_665802.1
		TRAF7	NP_115647.2
2	<i>Mus musculus</i>	TRAF1	NP_033447.2
		TRAF2	NP_001277342.1
		TRAF3	NP_035762.2
		TRAF4	NP_033449.2
		TRAF5	NP_035763.2
		TRAF6	NP_033450.2
		TRAF7	NP_001165584.1
3	<i>Bos taurus</i>	TRAF1	NP_001179730.1
		TRAF2	XP_002691752.2
		TRAF3	NP_001192515.1
		TRAF4	NP_001094750.1
		TRAF5	NP_001098810.1
		TRAF6	NP_001029833.1
		TRAF7	NP_001019692.1
4	<i>Gallus gallus</i>	TRAF1	XP_024997267.1
		TRAF2	XP_015135104.1
		TRAF3	XP_040557218.1
		TRAF4	XP_015151572.3
		TRAF5	NP_001383019.1
		TRAF6	XP_004941605.1

No.	Species name	Gene name	Accession no.
5	<i>Xenopus tropicalis</i>	TRAF7	NP_001012546.2
		TRAF1	XP_031747100.1
		TRAF2	XP_031746911.1
		TRAF3	XP_031746743.1
		TRAF4	NP_001005074.1
		TRAF5	XP_004914139.2
		TRAF6	NP_001008162.2
6	<i>Pelodiscus sinensis</i>	TRAF7	NP_001135502.1
		TRAF1	XP_025039277.1
		TRAF2a	XP_006134818.1
		TRAF3	XP_025038847.1
		TRAF5	XP_006131156.1
		TRAF6	XP_006124531.1
		TRAF7	XP_014432120.1
7	<i>Danio rerio</i>	TRAF1	NP_001121853.1
		TRAF2a	XP_005172003.1
		TRAF2b	XP_005165557.1
		TRAF3	NP_001003513.1
		TRAF4a	NP_991325.1
		TRAF4b	NP_997982.1
		TRAF5	XP_021325328.1
8	<i>Ictalurus punctatus</i>	TRAF6	NP_001038217.1
		TRAF7	NP_001073654.1
		TRAF1	XP_017322461.1
		TRAF2a	XP_017307574.1
		TRAF2b	XP_017315229.1
		TRAF3	XP_017332416.1
		TRAF4a	XP_017346543.2
9	<i>Oncorhynchus mykiss</i>	TRAF4b	XP_017348734.1
		TRAF5	XP_017333882.1
		TRAF6	XP_017313922.1
		TRAF7	XP_017312723.1
		TRAF1	XP_021461029.1
		TRAF2a	XP_021462083.2
		TRAF2b	XP_021458047.1
10	<i>Cyprinus carpio</i>	TRAF3	NP_001118087.1
		TRAF4	XP_021438221.1
		TRAF5	XP_021413078.1
		TRAF6	XP_036837353.1
		TRAF7	XP_036829480.1
		TRAF1	XP_042585371.1
		TRAF2a	XP_042579944.1
11	<i>Ctenopharyngodon idella</i>	TRAF2b	XP_042580991.1
		TRAF3	XP_042598390.1
		TRAF4a	XP_042595193.1
		TRAF4b	XP_018953598.1
		TRAF5	XP_018933195.1
		TRAF6	XP_042584118.1
		TRAF7	XP_042578737.1
		TRAF1	ABE99697.1
		TRAF2b	ABE99696.1
		TRAF3	AVR54984.1
		TRAF4b	QDF63034.1
		TRAF5	QDF63035.1
		TRAF6	AGI51678.1
		TRAF7	ULE28382.1

No.	Species name	Gene name	Accession no.
12	<i>Salmo salar</i>	TRAF1	XP_045562940.1
		TRAF2a	XP_014026490.1
		TRAF2b	XP_013990611.1
		TRAF3	XP_014048262.1
		TRAF4a	NP_001167069.1
		TRAF5	XP_014026273.1
		TRAF6	XP_045564128.1
13	<i>Takifugu rubripes</i>	TRAF7	XP_045571926.1
		TRAF2a	XP_011617744.1
		TRAF2b	XP_029693846.1
		TRAF3	XP_011618072.1
		TRAF4a	XP_003968588.1
		TRAF6	XP_029702628.1
		TRAF7	XP_003964369.1
14	<i>Sparus aurata</i>	TRAF2a	XP_030273274.1
		TRAF2b	XP_030292638.1
		TRAF3	XP_030299697.1
		TRAF4a	XP_030259023.1
		TRAF6	XP_030270209.1
		TRAF7	XP_030263764.1
15	<i>Oreochromis niloticus</i>	TRAF2a	XP_025752911.1
		TRAF2b	XP_013123763.1
		TRAF3	XP_025756743.1
		TRAF4a	XP_003440320.1
		TRAF5	XP_003452807.3
		TRAF6	XP_005455785.1
		TRAF7	XP_003446520.1
16	<i>Paralichthys olivaceus</i>	TRAF2a	XP_019949664.1
		TRAF2b	XP_019937631.1
		TRAF3	XP_019962478.1
		TRAF4a	XP_019944060.1
		TRAF6	XP_019955057.1
		TRAF7	XP_019967403.1
17	<i>oryzias latipes</i>	TRAF2a	XP_011477930.1
		TRAF2b	XP_004074805.1
		TRAF3	XP_004084442.1
		TRAF4a	XP_004075368.1
		TRAF5	XP_004065654.2
		TRAF6	XP_020567582.1
		TRAF7	XP_004071899.1
18	<i>Larimichthys crocea</i>	TRAF2a	XP_019119930.1
		TRAF2b	XP_010736878.2
		TRAF3	XP_027130745.1
		TRAF4a	XP_010747668.1
		TRAF5	XP_019128363.1
		TRAF6	XP_019128980.2
		TRAF7	XP_010741701.1

Supplementary Table S3. List of vertebrate species and the accession numbers of their TRAF nucleotide sequences used in this study

No.	Species name	Gene name	Accession no.
1	<i>Homo sapiens</i>	TRAF1	NM_005658.5
		TRAF2	NM_021138.4
		TRAF3	NM_003300.4
		TRAF4	NM_004295.4
		TRAF5	NM_001319207.2
		TRAF6	NM_145803.3
		TRAF7	NM_032271.3
2	<i>Gallus gallus</i>	TRAF1	XM_025141499.2
		TRAF2	XM_015279618.3
		TRAF3	XM_040701284.2
		TRAF4	XM_015296086.4
		TRAF5	NM_001396090.1
		TRAF6	XM_004941548.5
		TRAF7	NM_001012528.3
3	<i>Xenopus tropicalis</i>	TRAF1	XM_031891240.1
		TRAF2	XM_031891051.1
		TRAF3	XM_031890883.1
		TRAF4	NM_001005074.1
		TRAF5	XM_004914082.4
		TRAF6	NM_001008161.2
		TRAF7	NM_001142030.1
4	<i>Danio rerio</i>	TRAF1	NM_001128381.1
		TRAF2a	XM_005171946.4
		TRAF2b	XM_005165500.4
		TRAF3	NM_001003513.1
		TRAF4a	NM_205762.1
		TRAF4b	NM_212817.1
		TRAF5	XM_021469653.1
		TRAF6	NM_001044752.1
		TRAF7	NM_001080185.1
5	<i>Ictalurus punctatus</i>	TRAF1	XM_017466972.3
		TRAF2a	XM_017452085.3
		TRAF2b	XM_017459740.3
		TRAF3	XM_017476927.3
		TRAF4a	XM_017491054.3
		TRAF4b	XM_017493245.3
		TRAF5	XM_017478393.3
		TRAF6	XM_017458433.3
		TRAF7	XM_017457234.3
7	<i>Oncorhynchus mykiss</i>	TRAF1	XM_021605354.2
		TRAF2a	XM_021606408.2
		TRAF2b	XM_021602372.2
		TRAF3	NM_001124615.1
		TRAF5	XM_021557403.2
		TRAF6	XM_036981458.1
		TRAF7	XM_036973585.1

Supplementary Figure S1. Nucleotide and deduced amino acid sequences of open reading frames of *Pf*_TRAFs. (A) *Pf*_TRAF1, (B) *Pf*_TRAF2a, (C) *Pf*_TRAF2b, (D) *Pf*_TRAF3, (E) *Pf*_TRAF4a, (F) *Pf*_TRAF4b, (G) *Pf*_TRAF5, (H) *Pf*_TRAF6, and (I) *Pf*_TRAF7. The start and stop codons are marked in bold. The N-glycosylation sites are marked in black circles. The RING finger domain is indicated by the black box, the zf-TRAF domain by the middle bracket, the TRAF-BIRC3-bd domain by the double arrow, the coiled-coil domain by the underline, and the WD40 domain by the curly bracket. The letters e, c, t, and h denote extended strand, random coil, β -turn, and α -helix, respectively.

A

1 ATGGCTTTAGCAGCGCTGTGCCAGCTCCCCGGGAGAGAACGAATACCCGTCCGGTTTCCCGCAGAGCATCTGTGATGAAGTTCCGGCG
1 M A L A A P V P S S P G E N E Y P S G F P Q S I C D E V P A
c t t c c c c e e c c c c c
91 CAGAAATACTTGTGTACCCACTGTGACTGTGTGCTCAACGGAGCGCACCGGAGCAGTGGGACACCGCTACTGCTCGCGTGGCTTAC
31 Q K Y L C T H C D C V L N G A H R S T C G H R Y C L A C V H
h h h h h h h h h h h h h h h c c c c c c c c c c c c h h h h h
181 TGGCTCATCAGAAACAACAAAAATCTTGTGTGCACAAAGTGTAAAGAAGACCCAAACCAGCAAGGCAAGTACGGCTTACTGACTCTTGAC
61 W L I R N N K N L V C T K C K E D P N Q Q G K Y G L L T L D
h h e c h h h h h h h
271 CAGTTCCTCAACGACGAGCAATCAATAAAGAGATCCTGGCTCTGAAAGTGCACTGCACCAACACTAGCTGTACGTGGAAGAGCACCTTG
91 Q F F N D A A I N K E I L A L K V H C T N T S C T W K S T L
h c c c h h h h h h h h h h h h h h e e e c c c c t t c c h h h h
361 GAGGACTTTGAGGAGTATCAGTGTCTTGTGAATACGCTTTAATCCCTGCAACGTTGGCTGTGGGTTGATGTTTGGAGGAGCGTTG
121 E D F E E Y Q C H C B Y A L I P C N V G C G L M V L R K T L
h h h h h c c c c c c c e e e e c c c c c c c h h h h h h h h
451 GCTGCTCACCTGGACAAGGGCTGTCCCAATAATAAAGCTGTGTCTACATGTTCTGCCACTGACCCCTTCAGAACTCCAGAAACAT
151 A A H L D K G C P N N K S L C P T C S C P L T P S E L Q K H
h h h h h h c c c c c c c c c c c c c c c e e e h h h h c c c
541 GTGTGTCGCAACGACAAGTCTCTCAAAAGCAGAGAAACGACAGAGGATAATAAGCAAGCAAAATTCAGAAAGGAGTCAATGTCAG
181 V C P N D K K S S K A E K R Q K D N K Q A N S R R K E S C Q
c c c c c c c c c c h h h h h h h h h c c c c c c c c c c c
631 TTCTCTGACATTGGATGCCATTAAAGGGAAGCTAGAGAAATTGCGAGACCATGAAAGCTGCAGTTCCGCGGCCACCTTCAGCTCCTC
211 F S D I G C P F K G T V E K L R D H E S C S S A A H L Q L L
e e e e c c c c c c c c h h h h h h h h h h h h h h h h h
721 CTGGAGGTCTTCAGAAGTGTTCGGGTCTCTGTTCCTTCCCGCCTGAGAGGAGCGTGCACTTCCAGGCGCTGGACCTGCTCCTCCATGGC
241 L E V F R S V R V S V P S P P E R S V H F P G L D L L L H H
h h h h h h h h h h h h h h h h h h h c c c c h h h h h h h
811 CAGAGCTCACCTTCTGTTTGCACTCAATCGGCTGGTAGAGGACCGGATGGAGGAGTAAACGACATGGCACTCAGCCTT
271 Q S S P S V C T Q S A G E V E A D G M D G G V N D M A L S L
h h h h h h h h h h h h h h h h h h h c c c c c h h h h h h
901 CATGACGACCAAGCTGAGCTGGAAGTGGGCCAGCAGCTTCACGCCCTTCAGCAGAGGCTACAGATCAGGAGCAAGCTCATCTCGTACTC
301 H D D Q A E L E V G Q Q L H A L Q Q R L Q I M E N V I S V L
h
991 AGTCACGAGTGGAGAAACCCAGCTCACCGTGACAGCTCTGGACAGAGACCAACCAACATGACAGCTGGTGGAGCACTTAGACAGC
331 S H E V E K T Q L T V T A L D R D T N T N M Q L V E H L D S
h h h h h h h h h h h h h h h h h h h c c c h h h h h h h h
1081 GTGGTTGCAGATCAGCAGCAGAGGATGATCAGGAAAGACCTGCACATCGCCTGCTGCAGCAGAGCATCAGTGGCAGCAGGACGTGTC
361 V V A D Q Q Q R M I R K D L H I A S L Q Q S I S A Q Q D V S
h c
1171 TACGACGGCAGCTTCTCTGGAAGATCTGTAATGTCAGTCAGAAGTTAAGAGAGGACGACAGGGCAAAAGAGCAACCACTATTCGCCA
391 Y D G T F L W K I C N V S Q K L R E A A T G Q K S N Q Y S P
c t t e e e e e h h h h h h h h h h h h h h t t c c c e e c c c
1261 GCCTTCTATACATCCAGATATGGATTAAAGTGTGCATGCGGTGTACATAAACGGAGAGGAGTGGGAAAAGGACGACATGTCTCTT
421 A F Y T S R Y G F K V C M R L Y I N G D G V G K G T H M S L
c e e c c c c t t c e e e e e e e e e t t c c c c c c c c e e e
1351 TTCTTTGTGATTATGAGAGGAGAGTATGACCGCTTCTCTGTTGGCCTTTTAAACACAAGGTGACTTTCTTCTCATGACCAAGAACAA
451 F F V I M R G E Y D P L L S W P F K H K V T F F L I D Q N Q
e e e e e t c c t h h e e c c c c c c c c c e e e e e e c t t c
1441 AGAGAGCATGTACTCGACAGTTCCGTCCCGACCTCTCGTCCGTATCGTTCCAGCGGCCGTGCTGACATGAACGTGGCCAGCGGCTGC
481 R E H V L D T F R P D L S S V S F Q R P V S D M N V A S G C
c c h e e e h c
1531 CCTCTCTCTGCGCTGCGCAAGCTGCGCTCCCTGAAGCATGCGTACTGCAAGACGACACACTTTTATCAAGTGTGGTGGACTCT
511 P L F C P L A K L R S L K H A Y C K D D T L F I K C V V D S
c e e e e e c c c c c c c c c c c c c c c t t c e e e e e e c t
1621 TCATCTTGA
541 S S *
t c

B

1 **ATG**TTTCATTATAGCTCATGCTTTCTTTTCATCCCAATGCACTGAGCTCGGTTTCATTTCCCGGCTCAGGTCACATGCTCGCTCGGAATA
 1 M F H Y S S C F L S S Q C T E L G F I S R L R S H A R S G I
 e e c c c h e e e c c c c h h h h h h h h h h h h h
 91 ATAATGGCTGCACAGGAACCGTCCCTCGCTTCTACTGGAAGGCAACAAGCCGGCTTCCGAGGAAAAATCCTTGCCAACAAGCTGGAA
 31 I M A A Q E P S P S S L E G N K P G F P R K I L A N K L E
 e e e c c c c c c c c c c c c c c c t t c c c h h h h c c c c
 181 GAAAAGCATCTGTGTAACATCTGTCAGAAAACTACGAGGCGCTTTTCAGGCGCAGTGCAGGACACCGATTCTGTTCTACTGCTTTAAC
 61 E K H L **C N I C Q K I L R R P F Q A Q C G H R F C S Y C F** **(N)**
 h h h h h h h h h h h h h c c c c c c c c c c c c c c c h h h h h
 271 AAAACAGTGAGTTCTGGTCCCAAAAATGCAGTGTGTTATATAAGAAGATATATTGAGGAGCCAACATCGATTCTGAAACAGGGCTGT
 91 **K T V S S G P Q K C S A C** I K E D I F E E P T S I L K Q G C
 h e e c h h h h h h h h c
 361 GCITTTCTGACAACGCTGTAAGAGAGAAGTCGAAGCCTCGAAGCAGTTGTATCAACGAAGGCTGCAGCTGGACAGGAACCATCAAG
 121 A F P D N A A K R E V E A L E A V C I N E G C S W T G T I K
 c c c h h h h h h h h h h h h h e e e c c c c t t c c c h e e h h
 451 GAATATGAGGCTACCCAGAGGGACAGTGCAGATTTATGATCATCCCATGTCCTGCTCGAAAGAGCTCCTGAGAGCCAACGAACATTGAA
 151 E Y E A T **[H E G Q C D F M I I P C P S C K E L L R A N E L E]**
 h h h h h h h c c c c c e e e c c c c c c c c c c c c c h h h h h h h h
 541 CGTCACAACGAGCGGAATGCCAGAGAGGACTCTGAAGTCAAATACTGCAAAGAACCTTTTCATTTTAAAAACATTAAAGCCACGAT
 181 R H N E R E C P E R T L N C K Y C K E P F H F K N I K A H **[D]**
 h h h h h h h c h h h h h h h h
 631 GAGATTTGCCAAAATACCCAATGATTGTGAAGGCTGTGCGAAGAAGAAAATCCCAGAGAAAAGTACGTGGATCACATTAAAGCTGTGT
 211 E I C P K Y P M I C E G C A K K K I P R E K Y V D H I K L C
 h c h h h c c h h c c c c
 721 ACCAAAATCCGACCCCATGCAAGTTCAGTTCGCTGCGACATGTCGTGGAGAAGGAGAAGATCCATGAGCAGGCGGGCATGC
 241 T K F R T P C R F H V V G C D M S V E K E K I H E H **[E]** E R A C
 c h h h h h h h h h h h h
 811 TCGTACGAGCAGCTGAATCTGCTGCTGCACTTTATCATGGGCAAGGTAGCGTAGAGAGCCTGCAGCCGAGGGCCTGGAACCTGGCC
 271 S Y E H L N L L L H F I M G I K V S V E S L Q P Q G L E L A
 h
 901 AGCCACAAGCTCAAGGAGCTGCAGCAGTCTCTGTGCGAGCTGAAGTCAAGCTGGGTGAGCTGAGCGCTGGGGCTCCCGTGCAGGGGCC
 301 S H K L K E L Q Q S L C E L E V K L G Q L S A G A P V Q G P
 h
 991 TGTGTGCGGTGCGCGCTGCGCTAATCCTCCACCCCTGCGCCACCCGACCCACCCCTGACCACCTCGTTACCCCATTTGCCAGCGCT
 331 C V P C A P A P N P P P P A P P A P T L T T S F T P L P S A
 c h h c c c c c c c c c h h
 1081 GTCGGCGCGCCCTCGAGCTGCAACTGCACAGCGAGAAGACCAAGTGGCCGAGCTGAGCCGTGCTGCGCAGGCTGCGAGCTGAAGGCC
 361 V G A A L E L Q L H S E K T K V A **E L S R R C Q A**
 h
 1171 AGCACCTTGAGAACATTGTGTGCTGCTGAATGCGAGATGGAGCGCTCAGCCACCACCATGAGGCTTACAACCGCCAGCAGCGGCTC
 391 **S T F E N I V C V L N R E M E R S A T T M E A Y N R Q H R L**
 h
 1261 GACCAGGACAAGATCGAGATCCTCAACAACAGGTACGTCAGCTGGAGAGGACGGTGGGGCTGAGGGATCTTTCCATCGTGAGATGGAG
 421 **D Q D K I E I L N N K V R Q L E R T V G L** R D L S I V E M E
 c h
 1351 AGCAAGATGAGAGAAATGTCAGCCGCCACTACGATGGCGTGTGTTGTGGAGGATCAGGACTTTGCCAAGAAGAGGCAAGACGCTGA
 451 S K M R E M S A A T Y D G **V F V W R I T D F A K K R Q D A V**
 h h h h h h h h h h h c c t t e e e e e h h h h h h h h h h h h h h h h
 1441 GCTGGAAGGGCCCCAGCCATGTTCTACCTGCATTTTATACAAGCAAGTATGGCTACAAGATGTGTTGCGCATCTACCTGAATGGGGAT
 481 A G R A P A M F S P A F Y T S K Y G Y K M C L R I Y L N G D
 t t c c c c e e c c c c c c c c c c c c c c c c e e e e e e e e t t t t
 1531 GGAACAGGGCGCGCACTCACTTGTCTGTTCTGTTGTTGATGAGGGGACACAGTATGCTCAAGTGGCTTTTAAACAGAAG
 511 **G T G R G T H L S L F T G V V M R G H S D A L L K W P F N Q K**
 c c c c c c c h e e e e e e e e c c c c t h h h e c c c c c c t t t
 1621 GTCACCTGATGCTGCTGACCAAGATAACAGAGACATATTGACGCCCTCCGGCCGACATCTCGTCTCGTCTCCAGAGACCC
 541 V T L M L L D Q N N R E H I I D A F R P D I S S S S F Q R P
 e e e e e e c t t c c c h e e e e e c c c c c c c c c c c c c c
 1711 GTCAGCGACATGAACATGCGCAGCGGATGCCCTCTCTGTCGCCCTCCCTAAGCTGACTCCAAGAAGTACATACCTCGTGATGACACC
 571 V S D M N I A S G C P L F C P L P K L D S K N S Y I R D D T
 c c c c c c c c c c c c c e e e e h h h h c c c c e e e c t t c
 1801 ATCTTCATCAAGGCCATTGTTGACCTCACTGGCCCT**TAA**
 601 I F I K A I V D L T G L *
 e e e e e e e c c t t c

C

1 ATGCGACGTCCATCTTTGCCCTTCTTCGATGGACTCAACGTTACCAGGTATATCCCGGCAGGTCCTGTCCGTGCCATGGAACCTAAATAT
1 M A R P S L P S S M D S T L P G I S R Q V L S V S M E L K Y
c c c c c c c c c c c c c c c c c c c t t c c c c e e e c c c c h h h
91 CAGTGTCAAAAGTGCAAGGACGTTCTGAGGAAACCTTTCCAGGCGCAGTGTGGACATCGTTTCTGCGTGTCTGTTTAAACAACCTACC
31 Q C Q K C K D V L R K P F Q A Q C G H R F C V F C F K Q L T
h h h h h h h h h h c c c c c c c c c c c c c c h h h h h h h h
181 AGCTCTGGCCCAATTCCTTGGAAGCTTGTCGATGAAGGGATCTTTGAAGAAGAGCTCTCAATGCTCAACTTTTCTGTCGCTTTTCCA
61 S S G P I P C E A C R D E G I F E E E L S M L N F S V A F P
c h h h e e h h c c c c c
271 GACAATGCAGCAGCAAGAGAAATCGACAGTTTGCTGCTCAAAATGCCAATACGGCTGTTCCTGGGCAGGAACCTCTGAAGATTACGAG
91 D N A A R R E I D S L P A K C P N D G C S W A G T L K D Y E
t h h h h h h h h h h h h e c c c c c c t t c c c c h h h h h h
361 GGTCAAGCAGGAGGCGGATGTGAATTCGAGCGTGTCAGTGTGACGCGTGTCAAGTCATCATCTTCTCAGTGAGCGAGAGCGGCACAA
121 G Q H E G R C E F E R V K C D A C Q V I I L L S E R E R H N
h h h h c c c c h e e e c c c c c c c c h h h h h h h h h h
451 GAGAGAGGTGTGAAGCCCGTAACCTTAACGCAAACTGCAAAAGTTTCTTCAGCTTTAAAGATATCAAGGCTCATGATGAGATCTGT
151 E R E C E A R N L N C K Y C K V S F S F K D I K A H D E I C
h h c c c c c h h c c c c c c c c c c e h h h h h c c c c c c
541 TTAAATTTCCCAATGCAATGCAAGATTGTGGTAAAGAAAGATCCCGCAGAGAAAAGTTTCAAGAGCATAGCAATCTCTGCGCAAGTCT
181 L K F P M Q C K D C G K K K I P R E K F Q E H S K S C A K S
c h h h h h h h h h h
631 AAGATGCGCTGTAGTACAGCGAGATAGGCTGCAGAGCTGTGGTGGACAACGGAAGCAGCAGGAGCATGAACAGAGCAGTGTGATCGAG
211 K M A C Q Y S E I G C R A V V D N G K Q Q E H E Q S S V I E
c c c c c c c c c c c c c c c c h h h h h h h h h h h h h h h h
721 CACTTGGCGCTCATGTGCGCATGATCTGTCGGTGGCGCTCGACCCGAGCAGCGGAGAGTGGCAGGAGGACTCGGGTTTCGGCCTG
241 H L R L M L A M I S S V R P R P E A A G E W Q E D S G F G L
h h h h h h h h h h h h h h h h h c c c h h h h h h h h h h
811 TACCGGGCCCTGAAGACACGGTTCTTCCAGGCTCCAGGGTGCATCGGGAGACTCCTGCATGCAGCGGAAGATGACGCGCTGGAGAAC
271 Y R G P E D T V L P G S Q G A S G D S C M Q R K M T A L E N
h
901 ATCTGTGCGTGTGAACAGAGGTTGGAGCGCAGAGCTCTCAGGCTCGAAGCTCTTGAAGACAGCAGCGATCGACCGAGGAGATC
301 I V C V L N R E V E R T A L T L E A L G R Q H R L Q E K I
h
991 GAGAACCTATCCAACAGGTGCGTCAGTTGGAGCGGACGTTAACGATGCGAGATCTGCAACTCGCGAATCGGAACAGAAATTTGCGAGAG
331 E N L S N K V R Q L E R T L T M R D L Q L A E S E Q N L R E
h
1081 CTGCAGTTTTGTACGTTTCGATGGCGTGTTCATTGGAAAAATCTCCGATTTACCCGTCGCAGACAAGATGCTCTGGCTGGACGAGCGCT
361 L Q F C T F D G V F I W K I S D F T R R R Q D A L A G R A P
h h h h c c t t t e e e e e e h h h h h h h h h h h h h t t c c c
1171 GCCATGTTCTCGCCAGCATTCTACTCCAGTAAGTATGGCTATAAGATGTGTTTGAGGCTGTACCTGAACGGAGACGGTTCCGGGAAGAAAC
391 A M F S P A F Y S S K Y G Y K M C L R L Y L N G D G S G R N
e e c c c c c c c c c c c t t c e e e e e e e e e t t c c c c c c
1261 ACTCATCTCTCGCTGTTCTTTGTGGTATGAGAGGGAATACGACGCTCTACTCAATGGCCCTTCAGCCAGAGGTAACCTCTGATGCTT
421 T H L S L F F V V M R G K Y D A L L K W P F S Q K V T L M L
c c e e e e e e e e e t c c c h h e e c c c c c c c c e e e e e
1351 CTAGACCAGAATAACCGGAACACATCATCGATGCTTTACAGCTGACATCAGCTCCAGTCTTCCAACGCCATCATGAGATGAAC
451 L D Q N N R E H I I D A F R P D I S S T S F Q R P I S E M N
e c t t c c c h e e e e c c c c c c c c c c c c c c c c c c c
1441 ATAGCCAGCGGCTGTCCACTCTTCTGTCCACTGGCCAAGCTGGCAGGAAAAAGTTCCATGTCCGTGATGACACGATCTTATTAAAGCG
481 I A S G C P L F C P L A K L A G K S S Y V R D D T I F I K A
c c c c c c e e e e h h h h c c c c c e e c t t c e e e e e
1531 ATCGTAGATCTCACAGGACTTTAA
511 I V D L T G L *
e e c t t t c

[illegible]

E

1 **ATG**CCCGGCTACGACTATAAGTTCTGGAGAAGCCCAAGAGGCGCTTTCAGTGTCGCTGTGCAGTAAAGCCATGAGAGAACC GG TG CAG
 1 M P G Y D Y K F L E K P K R R F Q **C P L C S K A M R E P V Q**
 c t t c c e e e c c c c c c c h h c c c h e e e e c c c c c c e
 91 GTGTCGACCTGCGGCCACAGATTCTGCGACCTGCGTG CAGGAGTTCTCAGTGAGGGGTATTCAAGTGCCCCGAGGACCAGCTCCCC
 31 **V S T C G H R F C D T C L Q E F L S E G V F K C P E D** Q L P
 e c c c c c c c c c c c h h h h h h h h h c c c c c c c c c c c c c c c
 181 CTGGACTACGCTAAGATCTACCTGACCCGAGCTGGAGCAGCAGATCCTGGCTCTAGCTATCCGCTGCATCCACAGTGAGGAAGGCTGT
 61 L D Y A K I Y P D P E L E Q Q I L A L A I R C I H S E E G C
 c c h h h c c c c c c c h h h h h h h h e e e e c c c c c c c c c c
 271 CGCTGGACCGGCCAGATGAAGCAGCTGCAGAGCCATTCTCTACCTGTGCATTCAATGTGATCCCGTGCCCTAACCGCTGCAGCGTCAAG
 91 R W T G Q M K Q L Q S H F S T C A F N V I **P C P N R C S V K**
 c h h h h h h h h h h h h h c c c c c e e e c c c c c c c c c h
 361 CTGACACGCCGAGACCTGCCGAGCACCTGCAGCAGACTGCCCAAGCGCAAGGTCAAGTGGAGTTCTCGGCAGCGAGTTCACCGGC
 121 L T R R D L P E H L Q H D C P K R K V K C E F C G S E F T G
 h h h h h h h h h h h c c c c c e e c c c c c c c c c c h
 451 GAGGCTTCGAGAAATCACCAGGGCATTGTGCCAGGAGAGTGTATTGTGAGAACAAGTGTGGAGCGAGGATGATGAGGAGACTCCTG
 151 E A F E N H **Q G I C P Q E S V Y C E N K C G A R M M R R L L**
 h h h h h c c c c c c c c c c e e c c c c c c c c c c c c c h h h h
 541 GCCCAGCACACCATGTCTGAGTGTCCTCAACGACACAGCCATGCAAGTACTGCGGCAAGAGTTTGCTACGACCATCCAGAATCAT
 181 A Q H T M S E C P K R T Q P C K Y C G K E F V Y D T I Q N H
 h h h h h h c h h h h h
 631 CAGTACCACTGCCACGTTTCCAGTCCAGTGCCCAACCAAGTGTGGTGCCCCCAACATGCCCGTGAAGATCTCGCAACCCATGTAAAG
 211 **Q Y H C P R F P V Q C P N Q C G A P N I A R E D L A T H V K**
 h c h h h h h h h h
 721 GAAAGCTGCGGAGTCTTAGTGCTCTGTCCTTTAAGAAAGCTGGATGCAAGCATCGATGCCCAAGCTGGTGATGGCCGACACCTG
 241 E S C G S A L V L C P F K E A G C K H R C P K L V I G R H **L**
 h h h h h h h h h h h h h h h h h c c c c c c h h h h h h h h
 811 GAGGAAACCAAGTCCCACTTGACCATGATGTGCAACCTGGTAGGTGCTCAGCGGCAAGAGATCGCAGAGCTGCGGCGAGATCTGGAG
 271 E E T T K S H L T M M C N L V G R Q R Q E I A E L R R D L E
 h
 901 GAGCTGTAGTGAGCCATGATGGTGACTCATCTGGAAGTGAACGATTACTCAGCAAGTTGCAGGAGGCCAAATGCACAGCAACCAT
 301 E L S V S H D G V L I **W K L N D Y S R K L Q E A K M H S N H**
 h h h h h c c t t t c e e e e e h h h h h h h h h h h h h h h c c c c c
 991 GAGTTCTTCACTCCACCTTTTACACACCCGCTATGGCTATAAGCTGCAGGCATCCGCTTTCCTCAACGGCAACGGGAGCGGCGAAGGC
 331 **E F F S P P F Y T H R Y G Y K L Q A S A F L** **N** G N G S G E G
 e e e c c c c c c c c c c c c c c e e e e e e e e e e t t c c c c c c
 1081 TCACATCTCTCCGTCTACATCCGTGTGCTGCTGGCGAATACGACAACCTTCTCGAGTGGCCCTTTTCTACAAGGTCACTTTCTCCATT
 361 **S H L S V Y I R V L P G E Y D N L L E W P F S Y K V T F S I**
 c e e e e e e e e e c t t t c c h h h e c c c c c c c e e e e e e
 1171 ATGGACCAGAGTGATCCATCACTCTCCAAACACAGCACATCACTGAGACGTTCAACCCGAGCCCAACTGGAAGAACTTCCAGAAAACCC
 391 **M D Q S D P S L S K P Q H I T E T F N P D P N W K N F Q K P**
 e c c c c c c c c c c c h h h h e e e c c c c c c c c c c c c c c c
 1261 AGTGGCAGCCGAGCTCACTGGACGAGAGCGCACTAGGCTTTGGCTACCCCAAGTTCTCTCGCAGGAGGATCCGCAAGAGGAACCTAC
 421 **S G S R S S L D E S A L G F G Y P K F V S H E E I** R K R N Y
 c c c c c c c c c c c c c c c c c c e e e e h h h h c c c c c
 1351 ATCCGTGACAATGCTATCTTCTGAAGGCTCTATTGAGATCCCAAAAAGATCATGGCT**TGA**
 451 I R D N A I F L K A S I E I P Q K I M A *
 c c t t c e e e e e e e c c c c h e e h

F

1 **ATG**CCTGGTTTAGATTACAAGTTTCTGGAGCGACCGAGACGCCGCTTCTGTGTCCTTTGTGCAGTAAACCGATGAGGGAACCTGTCCAG
1 M P G L D Y K F L E R P R R R F L C P L C S K P M R E P V Q
c t t t c c h h h h c c c c h h h c c c c c c c c c c c c c c e e
91 GTGTCCACCTGCGGACACAGGTTCTGTGACACCTGTCTGCAGGAGTTTCTCAGTGCCGGCATATTCAAGTGCCAGAAAGATCAGATGCT
31 V S T C G H R F C D T C L Q E F L S A G I F K C P E D Q M P
e e c c c c c c c c c h h h h h h h h h t c c c c c c c c c c c c c
181 CTCGACTACGCTAAAAATTTCCAGATGTCGAGTTGGAGCAGCAGATTCTGGCTCTGCCATCCGCTGCATTACAGTGAGGAAGGTTGC
61 L D Y A K I F P D V E L E Q Q I L A L P I R C I H S E E G C
c c h h h e c c c h h h h h h h h h h e e e e c c c c t t c c
271 CGCTGGTCAGGACAGAATAAACAACACTACAGGTCCATCTCTCAGTATGTACCTATAACGTGGTCCGTGTCCAAACCGCTGCATGATGAAA
91 R W S G Q N K Q L Q V H L S V C T Y N V V P C P N R C M M K
c h h h h h h h h h h h h h h t c c c e e e c c c c c c c c h h
361 CTGTTGCGCCGTGATCTTCTCAGCACCTGCAGCATGACTGCACCAAGAGAAAGTCGCTGTGACCACTGCGTGTGATGAGTTACAGGG
121 L L R R D L P Q H L Q H D C T K R K L R C D H C A D E F T G
h h h h h h h h h h h c c c c c c c c c e e c c c c c c c c c h
451 GAAGCAGATGAGAGACACAGGACATGTATCCAGAGGAGAGTGTGTACTGTGAGAATAAGTGTGGGGCTCGTATGGTGGCAGGTGCTG
151 E A H E R H Q D M Y P E E S V Y C E N K C G A R M V R R L L
h h h h h c c c c c c c h h h h h h h h h h h h h h h h
541 ACGCAGCACAGCGTGTCGAAATGTCCTAAACGCAAAGTCTCTGCAAATACTGCAGCAAGGAGTTCCTGTACGACACCATTGAGAAATCAT
181 T Q H S V S E C P K R K L S C K Y C S K E F L Y D T I Q N H
h h h h h h h h h c c c c c c c c c c c c c c c c c c h h h h h h h h
631 CAGAGCCAGTGTCCACGCGTCCAGTGCAGTGTCTTAACAGCTGTGGCACACCCGGCATCCCGAGAGGATTTAACCATTTCATGTTAAG
211 Q S Q C P R V P V Q C P N S C G T P G I T R E D L T I H V K
c h h h h h h h h h
721 GAGAGCTGTGGGACCTCCATGGTCTGTCTTAAAGACGCGGCTGCAGATACAGATGCTCAAGCCTGCAGTGTCCCTTCACCTG
241 E S C G T S M V L C P F K D A G C R Y R C S K P A V S L H L
t t c c c c c e e e c c c c c c t t c c c c c c c c h h h h h h h
811 GATAGCCCGCTCACTCTACCTGTCTTACTCAGCAGCCTGTTTCTAGGCAGAGACTCGAGCTGCAAAAGCTGAGGCGTCGTTGTCGAG
271 D E A A H S H L S L L S S L V S R Q R L E L Q K L R R R V E
h
901 GAACCTTCCGGAACCAAGACGGGACTTTACTTTGGAAAAATCCCAACTACAGCCGTCACCTACAAGAAACAGAAATGCTCGAATGGA
301 E L S G T Q D G T L L W K I P N Y S R H L Q E T R N C S N G
h h h h c c c c c c e e e e h h h h h h h h h h h h h c c c c c
991 ACGTCGGAGCTCTTCAGCCCCGTTTCTACTCTCATCGCTACGGATACCGTCTCCAAGTTCGGTCTTTCCGAACGGGAACGGCAGCGGC
331 T S E L F S P V F Y S H R Y G Y R L Q V S V F P N G N G S G
c c e e e c c c c c c c c c c c c c c c e e e e e e e e c c c c c c
1081 GAAGGAACATACCTCTCCGTCTATATCAGAGTGTCCCGGGGAGTACGACGGCCTATTGGAGTGGCCGTTCCCTCACCAGCTCACCTTC
361 E G T Y L S V Y I R V L P G E Y D G L L E W P F P H R V T F
c c c e e e e e e e h c t t t c c c h h e c c c c c c c e e e
1171 TCGTGTGTGACCAGAGCGACCCAGTACTGTCCAAACCTCAACAGCTACCGGGAGCTTCAGCCAGATCCCAACTGGAAGAACTTCCAG
391 S L L D Q S D P V L S K P Q H V T G S F S P D P N W K N F Q
e e e c c c c c c c c c c c c c h e e e e c c c c c c c c c c c
1261 AGACCTCGACCTGGAGCAATCGGGAGCGTACGTACCAGCCTTTTGGACGAGAGTATGCTGGGATTGCGGTACCCCAAGTTTATCTCGCAC
421 R P R P G A I G S V R T S L L D E S M L G F G Y P K F I S H
c e e e c h
1351 GAGCAGATGAAGCAAAGGAACATACATCAGAGACAACGCCATCTTCATCAAAGCTTCTGTAGATGTGGTGACAGAGAATAATCAACTAA
451 E Q M K Q R N Y I R D N A I F I K A S V D V V Q R I I N *
h h h h h c c c c c t t c e e e e e e e c c c h h e e c

G

1 **ATG**GCAGCTGAGGAGAATGAATGCTTGAGCCTCCAGCTCTCAAAACAGAGCTCTGATCCTGTGAGGTCGTGGGAGTTGGAGTCTGTCCTG
1 M A A E E N E C L S L Q L S K Q S S D P V R S W E L E S V L
h h h h h c c c c h e e e c c c c c c c c c h h h h h h h h
91 GCCAATCGCACACTCAGTTTGTGTCGGGCTTGAGGAGCGCTACATGTGCCCGGCTGTGGTGACGCCATTCTTAACCCCCACCAGAGC
31 A **(N)** R T L S F V S R L E E R Y M C P A C G D A I L N P H Q T
h h h h h h h h h h h h h h h c c c c c c c e e e e c c c c c
181 GGCTGTGGCCACATCTTCTGTGCCAAGTGCATTAGAACGTTTATTGAGAGCCGCGACACATCCAAATGTCCCTTAGATGGCATTITTTGATC
61 G C G H I F C A K C I R T F I E S R D T S K C P L D G I L I
c c c c c e e c h h h h h h h h h c c c c c c c c c c c c c h e
271 AAGTCTGAGGAGGTTTTCAAGACAAGTGTGTAAGAGAACTACTAAATCTTGAAGTTTACTGTAGCAACACTCCAGATTGCACACAA
91 K S E E V F Q D N C C K R E L L N L E V Y C S N T P D C T Q
c h h h h h c c c c c c c h h h h h e e e e e e c c c c c c c c c
361 AAAGTGCTCTGTGTAATTTGAGAAACACCTAAGTCTTTGTCAGTATGAGACCTGCAATGCTCAACCCCGGCTGCACTGACATCCTG
121 K V P L C N L Q K H L T L C Q Y E T L Q C S N P G C T D I L
h e e h h h h h h h h h c c c c c h h e e c c c c c t t c c h h h
451 TTACGCAAGAAATGACCAGACCAGCGAAACCTGTGTCAGTTTCGACAGAGTTCTGTACTATTGCACAAGCCATACCTATTACC
151 L R K N V P D H Q R N L C Q F R T E F C H Y C T K P Y P I T
h h h h h h h h h h h h h c c c c c c c c c c c c c c c c h h
541 CAGTCCAGGACCATGAACAGATGTCATGCCCTGAAGCAGAGCTTCAGTGTCCCAATAACTGCTCTCAGATGGTTAAGAGGCATAAGCTC
181 Q L Q D H E Q M S C P E A D V Q C P N N C S Q M V K R H K L
h h h h h h h h h c c c c c c c c c c c c c c c c c h h h
631 AAAGGACATATAGATGAGTCCAGAAGTGGAGACAGACTGTATTATAAGCAATATGGCTGCACAGTCCGAGATAAACGAAGCAAAGTG
211 K G H I D E C P E V E T D C I Y K Q Y G C T V R D K R S K V
h h h h h c c c c c c c c c c c c c c c e t c c c c e e c c c h h h
721 AAAGTCCATGAATACACTGAATTTAGCCATCATGTGCTACTTGTACTGGAGAGCAACAGCAAGCTTGTAAACAGGTAGACCAGCTGCAG
241 K V H E Y T E F S H H V L L V L E S N S K L A K Q V D Q L Q
h
811 CAGGACTTGGCCCTCCAGGAGAGGGAGCTGAAAGAGAGAAACTTGTCTTGTGTAACCTTAACAGGAGATGACCAAGTGTGACAGCGCA
271 Q D L A L Q E R E L K E R N L L V A N L N R E M T K C D S A
h
901 TTTCTGCAATTGAGAGGTCAGTGGTGGAGCAGAGGCGCTCTCAAGCGTTAAACAGGAGCTGCAGGAGTTGCGTAATGTTCTGGAT
301 S S A I Q R S V V E Q R E S V S S V K Q E L Q E L R N L D
h
991 GCTGAGCTGGCTAAAGAGGAGCTGAGTGATCTCCGAGCTTCACTGCACTCTCTCAGACAGCAAGTGGCAATGACACAGAGCCTCAGAGAT
331 A E L A K E E L S D L R A S L D S L R Q Q V A M T Q S L R D
h
1081 CACCTGGGAGCTTTAGGTCAGACATGTCAGCGTCACACTCGACTACTGGACATCCATGTGGAGCAGCTGCAGTGAACGAGCAACGTTTT
361 H L G A L G Q T C Q R H T R L L D I H V E Q L Q C N E Q R F
h
1171 CGCCAAGTGTGACGTCATATGATGAAAACTCATCTGGAAGATTCTGGACTACCAGCGTAGAAAAAGCGTGGTGACCCGCTCACC
391 R Q L E S T S Y D G K L I W K I L D Y Q R R K D A G A P L T
h h h h h h h c c t t t c e e e e e h h h h h c c c h h c c c c
1261 TCACCGCCTTTTACACCGGCCGAGTGGCTACAAGCTGAGTGGCCGTGCGTACCCGGATGGGGACGGAAGCGCCGAGGCACACCTT
421 S P P F Y T G R S G Y K L S A R A Y P D G D G S A R G T H L
c c c c c c c c c c c c c e e e e e e e e t t t t c c c c c c c e
1351 TCTCTACATCATGGTGATGAGAGGTGACTTCGACTCACTGCTGCCGTGGCCATTTCGCCAGAGCGTCACACTCACCGTGTAGACCAG
451 S L Y I M V M R G D F D S L L P W P F R Q S V T L T V L D Q
e e e e e e e t t t t t c h e e c c c c c c t t e e e e e e c t
1441 AGTGGCTCAGCAACACGTCAGCTGCAGCTTACCCCTGACACCAGCAAAGAGAGCTTCGCCAGACCCACAGCTGACAGCAACGCGCGG
481 S G S R N H V S C S F T P D T S K E S F R R P T A D S N A A
t c c c c c e e e e c c c c c c c c c c c c c c c c c c c
1531 TTAGGGTTCTCTCGCTTCTCTCAGACTGACCTGGAAGGTCCCGAAAAGCCATCTTCATACGAGATGACACTCTGTTTGCAAGGTT
511 L G F S R F I S H T D L E G P R N A I F I R D D T L F V K V
t t c c e e e e e h c c c c c c c t t c e e e c t t c e e e e e
1621 AAGGTTGACACAAACAGGGTTGGAGGATTG**TAG**
541 K V D T T G L E D L *
e e c c c c c c t h

H

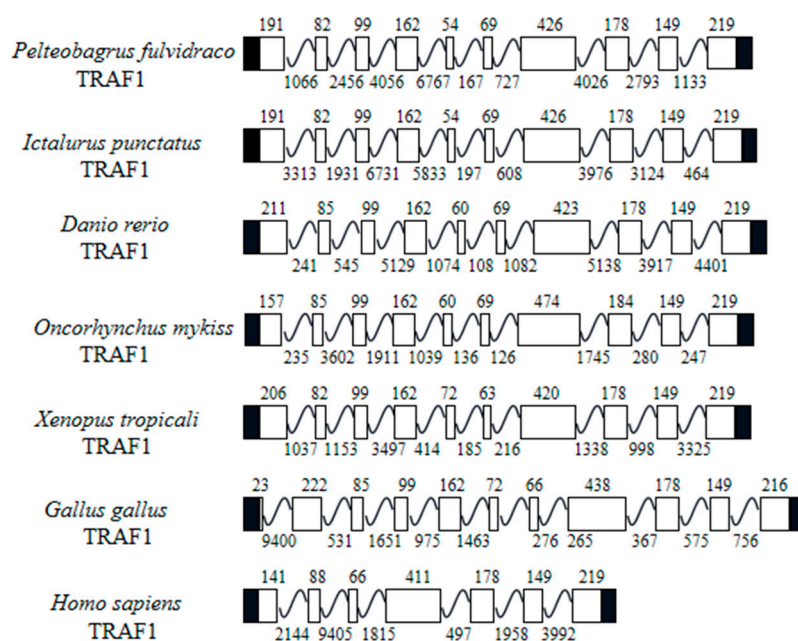
1 ATGGCATCATGATAGTACATGCACAAATCCAATCCAGATGAGTATCCATCATCCAGATGATGGCTGATATGGAGAAGGAGTCGTATCTA
1 M A S C S D M H K S N P D E Y P S S R C M A D M E K E S Y L
c c c c c h h c c c c c c c c c h h h h h h h h t t c c e e
91 AGCCCTACAGATAGCCCATCTACAATTAGTGTCTCATCCAACATCCAGGAACAGCAAGGCTATGATGTTGAATTTGATCCCCACTGGAG
31 S P T D S P S T I S V S S N I Q E Q Q G Y D V E F D P P L E
c c c c c c c e e e c
181 AGCAAGTATGAATGTCCCATCTGCCTGATGGGTCTACGGTCAAGTGTGCAGACACCATGTGGTCATCGCTTCTGTAACAGTTGTATTAAA
61 S K Y E [C P I C L M G L R S A V Q T P C G H R F C N S C I K]
c c c c c c c e e e e e e e c c c c c c c c c c c c c c c c h h h h h
271 AAATCCATCAGGGACAGGGGCAAAAATGTCCAGTTGACAATGAGGTGCTGACAGAGGACCAGCTTTTCCAGATAACTTTGCCAAGAGG
91 [K S I R D T G Q K C P V D] N E V L T E D Q L F P D N F A K R
h h h c h h h h h
361 GAAATCCTGTCTCTTACTGTACGCTGCCGAATGTTAGCTGTAGTGACATAATGGAGCTCAGGCACCTGGAGAATCACTTGAAGCTATGT
121 E I L S L T V R C R [N] V S C S D I M E L R H L E N [H L K L C
h h h e e e e e c c c c c c c c c c h h h h h h h h h h h c c c
451 AAATTTGCTACAGTGCCTTGTCCCCAGTGTAGAGGCTGTATGGAAGAATAGTATAGAGGACCATATGAATCAGGACTGTTTACAGGCT
151 K F A T V P C P Q C Q R P V W K N S I E D H M N Q C D C L Q R
c e e e e c c c c c c c c c c h h h h h h h h h h h h h h h c c c c
541 CTGATCATATGCCCTGACTGTGCAGAGGGTATCATCTATGCTGACAAACAGTTTCATGAGCAGATGTGCCCTTGTGAATACAGTGTGT
181 L I T C P D C A E G I I Y A D] K Q F [H E Q M C P F V N T V C
c c c c c c c c c c c c c c h h h h h h h h c c c c c c c c c c
631 GAGTACTGTGGAATGATTAAATTCGGGGTCAGTTGTCTACACTGTGCCACAGACTGCCTGAAAGCTCCTGTTCCTGTACGTTCACAC
211 E Y C G M D L I R G Q L S S H C A T D C L K A P V A C T F N
c c c c c c c c c c h h h h h h h c c c c c c c c c c c c c c c c
721 ATATTTGGCTGTCAAGAAAAGATGCCGAGGAACAACCTGGCCCTTCACATGCAGGAGTTTACACGGATGCACATGCGTTTCATGGCTGAC
241 I F G C Q E K M P R N N L A L H] M Q E F T R M H M R F M A D
c c c c c h h h c c h
811 TTCCTGAGGAATCAGAGTGTGAATGGCATTCTCCCGCTCCAAAATGTGGCCCTTCATGTTACCCCCATCCGAACATGGTCCAGTTCC
271 F L R N Q S V N G I L P A P K C G P S C S P P S E H G A S S
h h h h h h h h h h h c c c c c c c c c c c c c c c c c h h c c c
901 AGGGTGGGAGCCATGTAGTGCAGCCAGGACATGCAGCAGTTACGTGAGACTGTTGTGGAACITGAGGGCCGCTCGTGCGCAGGAC
301 R V G E P C Q C S Q D M Q Q L R E T V V E L E G R L V R Q D
c c c c h
991 CACCAGTTACGGGAGCTGAGCATTGCAATGATACACAGCATAACAGATAACGGAGCTACGCAAGAAGCTGGCATCGCTGGAAGAGAAA
331 H Q L R E L S I R N D T Q H T Q I T E L R K K L A S L E E K
h
1081 ATGCACGAGCTGGAAGCTCAGCAGTACCAGGGTGTTTATGTATGGCGATTAGAGGGATTCTCAGCTCACCTGCAACAACAGAGCAGGA
361 M H E L E A Q Q Y Q G V Y V W R L E G F S A H L Q Q Q E A G
h h h h h h h c c t t t e e e e e e h h h h h h h h h h h h t t
1171 CAACCAGTAGTGTCCATAGCCACCATTTACACAGGAAAGCCAGGGTATAAGCTGTGCCTGCGACTGCACCTTCAGACACCCAGCGCG
391 Q P V V L H S P P F Y T G K P G Y K L C L R L H L Q T P S A
c c e e e c c c c c c c c c c t t c e e e e e e e e e c c c c c
1261 CCACGTTGCTCTAACTATATCTCATTGTTTGTGCATACTATGCAAGGAGAAATTTGACAGCCAGCTACCGTGGCCCTTCAGGGCAACATC
421 P R C S N Y I S L F V H T M Q G E F D S Q L P W P L Q G N I
c c c c c h e e e e e e e h t t c c c c e e c c c c c c c c e
1351 CGATTGTCTGTGCTGACAGGCTGAGGGCCAACACCACTGAGATAATGGAACCAACACAGACCTTCAGGCCTTCCAAAGGCCCACT
451 R L S V L D Q A E G Q H H T E I M E T K P D L Q A F Q R P T
e e e e e c c c c c h h h h h h h c c c c c c c c c c c c c
1441 ATGCAGCGCAACCCAAAGGCTTCGGCTATGTCACATTATGTCAGTTGAGGCAATTGCGCCAGCGTGGTTTGTAGGGGTGATGTGCTG
481 M Q R N P K G F G Y V T F M Q L Q A L R Q R G F V R G D V L
c c c c c c c c e e e e h h h h h c c c c c c c t t c e
1531 CTAGTGCCTGTGAGGTCATGCCTCGCTTTGACACAAGCCTTAGAAGAGAGGGCATGCAACCTCGAGAACCTGAACCATCTCTCTGA
511 L V R C E V M P R F D T S L R R E G M Q P R E P E P S L *
e e e e e c c c c c c h h h c t t t c c c c c c c c c c

1

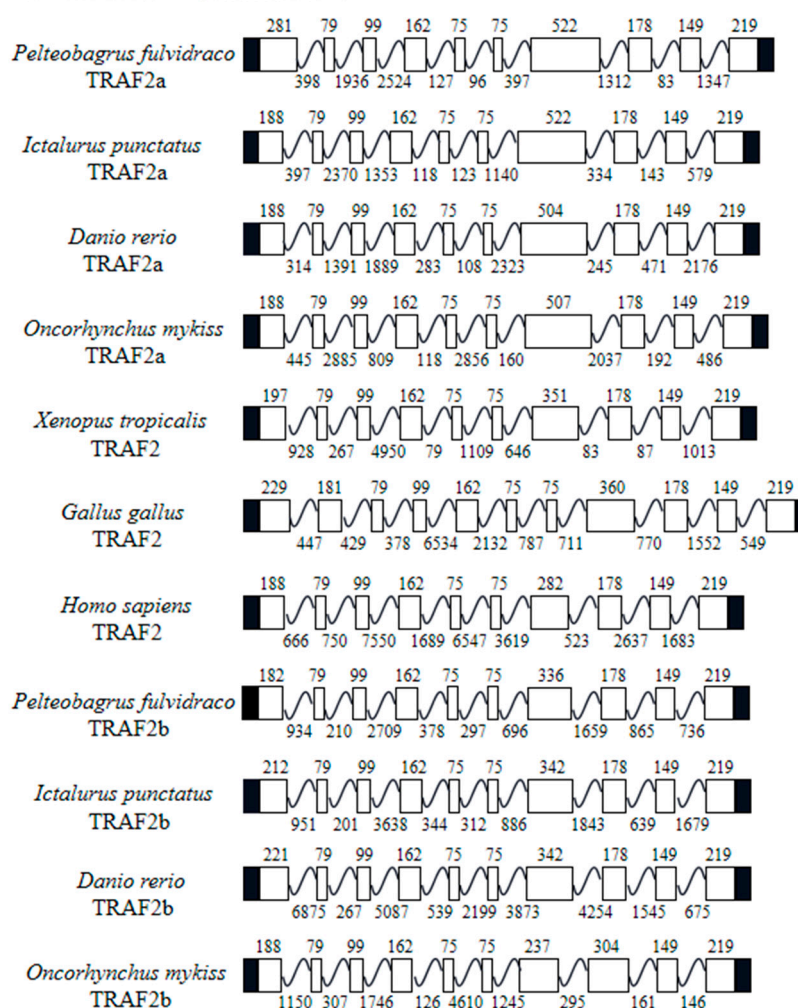
[illegible]

Supplementary Figure S2. Comparison of the gene organization of TRAFs genes in fish and tetrapods. Exon-intron structure of TRAFs from seven different vertebrate species: *Homo sapiens*, *Gallus gallus*, *Xenopus tropicalis*, *Oncorhynchus mykiss*, *Danio rerio*, *Ictalurus punctatus* and *P. fulvidraco*. The black boxes represent untranslated region, the white boxes represent exons, and the lines represent introns. The GenBank accession numbers of the TRAF nucleotide sequences are listed in Supplementary Table S3.

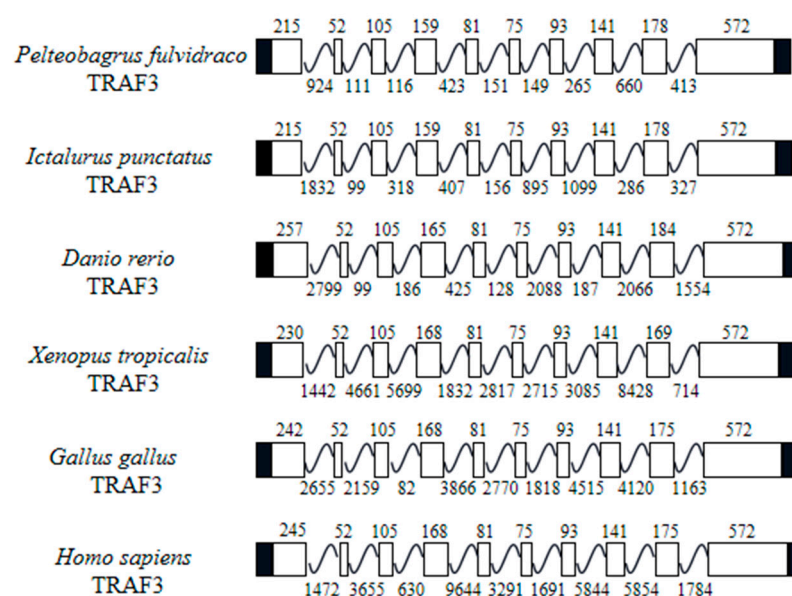
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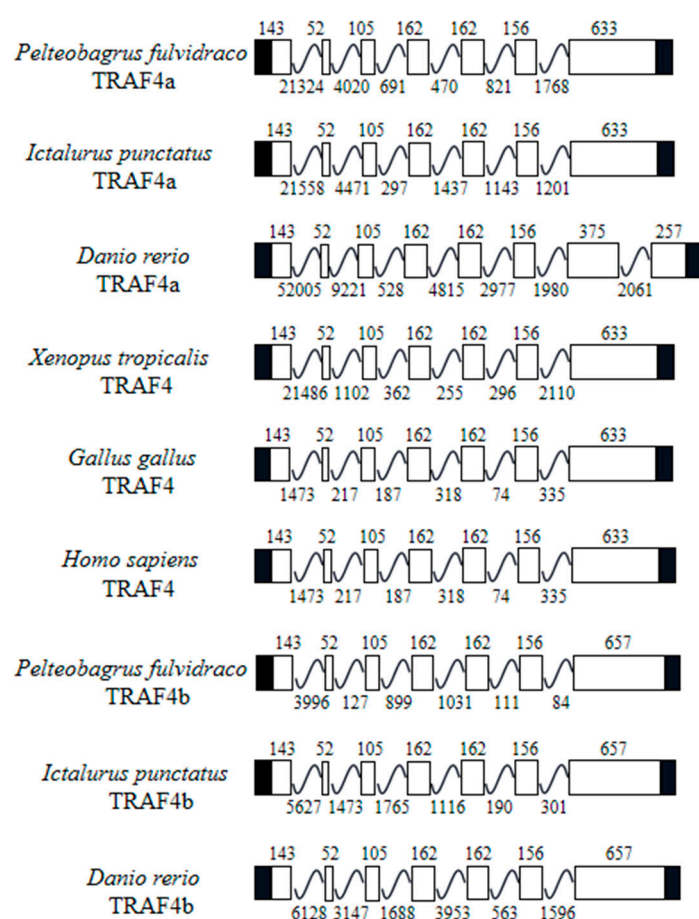
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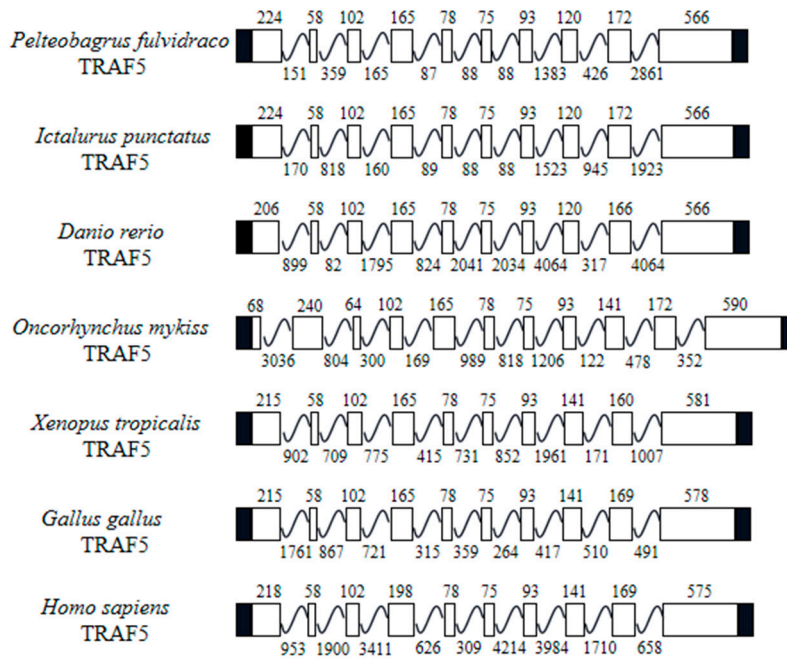
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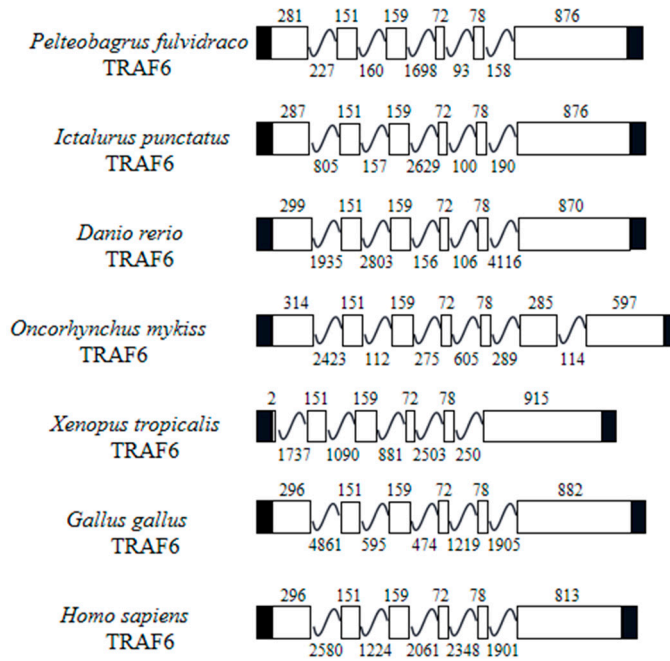
D:TRAF4a & TRAF4b



E:TRAF5



F:TRAF6



G:TRAF7

